

(FILE 'USPAT' ENTERED AT 13:57:50 ON 22 SEP 1999)

L1 7802 S CHEMICAL SYNTHESI?

L2 435 S L1(3A) (PROTEIN? OR POLYPEPTIDE?)

L3 26 S DHH

L4 5 S DESERT HEDGEHOG

L5 4 S L3 AND DESERT

L6 5 S L4 OR L5

L7 1 S L4(8A) (HUMAN OR HOMO)

FILE 'MEDLINE' ENTERED AT 13:49:05 ON 17 SEP 1999

FILE LAST UPDATED: 13 SEP 1999 (19990913/UP). FILE COVERS 1960 TO DATE.

MEDLINE has been reloaded to reflect the annual MeSH changes made by the National Library of Medicine for 1999. Enter HELP RLOAD for details.

OLDMEDLINE, data from 1960 through 1965 from the Cumulated Index Medicus (CIM), has been added to MEDLINE. See HELP CONTENT for details.

Left, right, and simultaneous left and right truncation are available in the Basic Index. See HELP SFIELDS for details.

THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE SUBSTANCE IDENTIFICATION.

=> s human(8a) (hedgehog or Dhh)

6684886 HUMAN  
1274 HEDGEHOG  
18 DHH  
L4 28 HUMAN(8A) (HEDGEHOG OR DHH)

=> s l4 and desert

2184 DESERT  
L5 1 L4 AND DESERT

LOCUS (LOC) : HSU59748 GenBank (R)  
 GenBank ACC. NO. (GBN) : U59748  
 CAS REGISTRY NO. (RN) : 178296-28-1  
 SEQUENCE LENGTH (SQL) : 285  
 5 MOLECULE TYPE (CI) : mRNA; linear  
 DIVISION CODE (CI) : Primates  
 DATE (DATE) : 4 Jul 1996  
 DEFINITION (DEF) : \*\*\*Human\*\*\* \*\*\*desert\*\*\* \*\*\*hedgehog\*\*\*  
 (hDHH) mRNA, partial cds.  
 10 SOURCE: \*\*\*human\*\*\* .  
 ORGANISM (ORGN) : \*\*\*Homo sapiens\*\*\*  
 Eukaryotae; mitochondrial eukaryotes; Metazoa;  
 Chordata; Vertebrata; Eutheria; Primates; Catarrhini;  
 Hominidae; \*\*\*Homo\*\*\*  
 15 NUCLEIC ACID COUNT (NA) : 62 a 73 c 92 g 58 t  
 REFERENCE: 1 (bases 1 to 285)  
 AUTHOR (AU) : Drummond, I.A.  
 TITLE (TI) : \*\*\*Human\*\*\* \*\*\*desert\*\*\* \*\*\*hedgehog\*\*\*  
 JOURNAL (SO) : Unpublished  
 20 REFERENCE: 2 (bases 1 to 285)  
 AUTHOR (AU) : Drummond, I.A.  
 TITLE (TI) : Direct Submission  
 JOURNAL (SO) : Submitted (02-JUN-1996) Renal Unit, Mass. General  
 Hospital, 149 13th street, Charlestown, MA 02129, USA  
 25 FEATURES (FEAT) :  

Feature Key	Location	Qualifier
source	1..285	/organism="Homo sapiens"
		/tissue-type="kidney"
		/dev-stage="15 week fetus"
gene	1..285	/gene="hDHH"
CDS	<1..>285	/gene="hDHH" /note="secreted protein" /codon-start=3 /product="desert hedgehog"

 30  
 35

/db-xref="PID:g1401272"  
/translation="IIFKDEENSGADRLMTERCK  
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WDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLL  
ARLAVEAGFDWVYYGS"

5

SEQUENCE (SEQ) :

1 atattatTTT taaggatgaa gagaacagtg gagccgaccg cctgatgacc gagcgttGta  
61 aggagcgggt gaacgcttG gccattGCCG tGatgaacat gtggcccgga gtgcgcctac  
10 121 gagtgactga gggctggac gaggacggcc accacgctca ggattcactc cactacgaag  
181 gccgtgctt ggacatcact acgtctgacc gcgaccgcaa caagtatggg ttgctggcgc  
241 gcctcgcaGt ggaagccggc tttgactggg tctactacgg atccg

GN HEDGEHOG.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TATE G., ENDO Y., MITSUYA T.;  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL; AB010994; D1025788; -.  
DR EMBL; AB010581; D1025788; JOINED.  
DR EMBL; AB010993; D1025788; JOINED.  
SQ SEQUENCE 396 AA; 43577 MW; 8200C40F CRC32;

Query Match 99.7%; Score 1800; DB 2; Length 396;  
Best Local Similarity 99.5%; Pred. No. 1.5e-159;  
Matches 372; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPYN 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 23 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPYN 82

Qy 61 PDIIFKDEENSGADRLMTERCKERNALAIAVNMWPGVRLRVTEGWDLEGHHAQDSLHY 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 83 PDIIFKDEENSGADRLMTERCKERNALAIAVNMWPGVRLRVTEGWDLEGHHAQDSLHY 142

Qy 121 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGGCFPG 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 143 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHVHVSVKADNSLAVRAGGCFPG 202

Qy 181 NATVRLWSGERKGLRELHRGDWVLTADASGRVVPTPVLLFLDRDLQRRASFVAVETEWPP 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 203 NATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQRRASFVAVETEWPP 262

Qy 241 RKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRA�DSVLAPGGDALRPARVARVAREEAV 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 263 RKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRA�DSVLAPGGDALRPARVARVAREEAV 322

Qy 301 GVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLHALGALLPGGAVQPTGMHW 360  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 323 GVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLHALGALLPGGAVQPTGMHW 382

Qy 361 YSRLLYRLAELLG 374  
||| ||| ||| |||  
Db 383 YSRLLYRLAELLG 396

; Patent No. 5789543: COMPARISON TO SEQ ID NO:3  
; GENERAL INFORMATION:  
; APPLICANT: Ingham, Phillip W.  
; APPLICANT: McMahon, Andrew P.  
; APPLICANT: Tabin, Clifford J.  
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
; TITLE OF INVENTION: Proteins and Uses Related Thereto  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,427B  
; FILING DATE: 30-DEC-1993  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-176-427B-4

Query Match 96.8%; Score 1851; DB 2; Length 396;  
Best Local Similarity 96.5%; Pred. No. 5.6e-202;  
Matches 382; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MALLTNLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS 60  
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Db 1 MALPASLLPLCCLALLALSAQSCGPGRGPVGRRYVRKQLVPLLYKQFVPSMPERTLGAS 60

Qy 61 GPAEGRVARGSERFRDLVPNYPDIIFKDEENSGADRLMTERCKERVNALAIAVNMWPG 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 GPAEGRVTRGSERFRDLVPNYPDIIFKDEENSGADRLMTERCKERVNALAIAVNMWPG 120

Qy 121 VRLRVTEGDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN 180  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 121 VRLRVTEGDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN 180

Qy 181 HIHVSVKADNSLAVRAGGCFFGNATVRLWSGERKGLRELHRGDWVLTADASGRVVPTPVL 240  
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Db 181 HIHVSVKADNSLAVRAGGCFFGNATVRLRSGERKGLRELHRGDWVLAADAAGRVVPTPVL 240

Qy 241 LFLDRDLQRRASFVAVETEPPRKLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV 300  
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Db 241 LFLDRDLQRRASFVAVETERPPRKLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV 300

Qy 301 LAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL 360  
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Db 301 LAPGGDALQPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL 360

Qy 361 RLLHALGALLPGGAVQPTGMHWYSRLLYRLAELLG 396  
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Db 361 RLLHALGALLPGGAVQPTGMHWYSRLLYRLAELMG 396

AC 043323; COMPARISON TO SEQ ID NO:3  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE HEDGEHOG.  
GN HEDGEHOG.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TATE G., ENDO Y., MITSUYA T.;  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL; AB010994; D1025788; -.  
DR EMBL; AB010581; D1025788; JOINED.  
DR EMBL; AB010993; D1025788; JOINED.  
SQ SEQUENCE 396 AA; 43577 MW; 8200C40F CRC32;

Query Match 99.7%; Score 1908; DB 2; Length 396;  
Best Local Similarity 99.5%; Pred. No. 2.4e-168;  
Matches 394; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALLTNLLPLCCLALLALPAQSCGPGRGPGVGRYYARKQLVPLLYKQFVPGVPERTLGAS 60  
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Qy 61 GPAEGRVARGSERFRDLVPNYPDIIFKDEENSGADRLMTERCKERVNALAIAVNMWPG 120  
Db 61 GPAEGRVARGSERFRDLVPNYPDIIFKDEENSGADRLMTERCKERVNALAIAVNMWPG 120

Qy 121 VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSRDRNKYGLLARLAVEAGFDWVYYESRN 180  
Db 121 VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSRDRNKYGLLARLAVEAGFDWVYYESRN 180

Qy 181 HIHVSVKADNSLAVRAGGCFFPGNATVRLWSGERKGLRELHRGDWVLTADASGRVVPTPVL 240  
Db 181 HVHVSVKADNSLAVRAGGCFFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVL 240

Qy 241 LFLLDRDLQRRASFVAVETEWPPRKLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV 300  
Db 241 LFLLDRDLQRRASFVAVETEWPPRKLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV 300

Qy 301 LAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL 360  
Db 301 LAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPL 360

Qy 361 RLLHALGALLPGGAVQPTGMHWYSRLLYRLAEELLG 396  
Db 361 RLLHALGALLPGGAVQPTGMHWYSRLLYRLAEELLG 396

L3 ANSWER 1 OF 8

GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AI666359 GenBank (R)  
GenBank ACC. NO. (GBN): AI666359  
CAS REGISTRY NO. (RN): 232155-01-0  
SEQUENCE LENGTH (SQL): 463  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Expressed sequence tag  
DATE (DATE): 12 May 1999  
DEFINITION (DEF): mullg06.x1 Soares 2NbMT Mus musculus cDNA clone  
IMAGE:639130 3' similar to TR:Q61488 Q61488  
DESERT HEDGEHOG HOMOLOG  
PRECURSOR ;, mRNA sequence.  
KEYWORDS (ST): EST  
SOURCE: house mouse.  
ORGANISM (ORGN): Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
Murinae; Mus

NUCLEIC ACID COUNT (NA): 87 a 124 c 138 g 113 t 1 others

COMMENT:

Other\_ESTs: mullg06.y1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watsen.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 261.

REFERENCE: 1 (bases 1 to 463)

AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;  
Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;  
Allen,M.; Bowers,Y.; Person,B.; Swaller,T.;

Gibbons,M.;

Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.; Kohn,S.;  
Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;  
Waterston,R.; Wilson,R.

TITLE (TI): The WashU-NCI Mouse EST Project 1999

JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..463	/organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGGCGCGTTT TTTTTTTTTTTTTTTTTTTTT 3']";

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /db-xref="taxon:10090" /clone="IMAGE:639130" /clone-lib="Soares 2NbMT" /sex="male" /tissue-type="Thymus" /dev-stage="4 weeks" /lab-host="DH10B"

SEQUENCE (SEQ):

1 ttttttgctt tcctgaaggg tggatgatgaag gagatctcac tttatTTTttt tagTTTtag  
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121 tgggtgggtgt gtagagcagg tggggagaaa ctctccttac ctctgtcatc aggcggctcg  
181 cggcgctgtt ctccatcc ttgaagatta tgcgggggtt gtagttgggt acgaggtccc  
241 ggaagcgctc cgacccttcc gttaccctcc cctccgctgg cccactcgcg cccagggtcc  
301 gctcgccatc actgggcaca aactgcttgt atagcagagg cacaagttgc ttgcgcacat  
361 tacgcccncg gccacccgggt tctcgcccg gcccgcagct ctggcagat agtgcacaaga  
421 gtgccaagca gcacaggggc aacagactgg cccgcagagc cat

L3 ANSWER 2 OF 8

GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AI645932 GenBank (R)  
GenBank ACC. NO. (GBN): AI645932  
CAS REGISTRY NO. (RN): 231418-84-1  
SEQUENCE LENGTH (SQL): 537  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Expressed sequence tag  
DATE (DATE): 29 Apr 1999  
DEFINITION (DEF): mul1g06.y1 Soares 2NbMT Mus musculus cDNA clone  
IMAGE:639130 5' similar to TR:Q61488 Q61488  
**DESERT HEDGEHOG HOMOLOG**  
PRECURSOR ; mRNA sequence.  
KEYWORDS (ST): EST  
SOURCE: house mouse.  
ORGANISM (ORGN): Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;  
Murinae; Mus  
NUCLEIC ACID COUNT (NA): 107 a 159 c 164 g 107 t  
COMMENT:  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsen.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco  
High quality sequence stop: 478.  
REFERENCE: 1 (bases 1 to 537)  
AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;

Gibbons, M.;

Wylie, T.; Underwood, K.; Steepe, M.; Theising, B.;  
Allen, M.; Bowers, Y.; Person, T.; Swaller, T.;

TITLE (TI):

The WashU-NCI Mouse EST Project 1999

JOURNAL (SO):

Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..537	/organism="Mus musculus" /strain="C57BL/6J" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'. TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTT TTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /db-xref="taxon:10090" /clone="IMAGE:639130" /clone-lib="Soares 2NbMT" /sex="male" /tissue-type="Thymus" /dev-stage="4 weeks" /lab-host="DH10B"

SEQUENCE (SEQ):

1 cactcaccct cgaccaccc gctctgtaaa tggtagtcta tcagtagtag gttggagggtt  
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121 tactctggga ctttctctat ctgcgggtgtt cttagtcc tgcggagatg cccaaattgac  
181 aggagagcca gtgaggacaa gaacgctccc ttccgaccac agtccacggc acccatggct  
241 ctgcccggcca gtctgttgcc cctgtgtc ttggcactatc tggactatc tgcccagagc  
301 tgcggggccgg gcccggggacc ggttggccgg cggcggtatg tgcgcggca acttgtgcct  
361 ctgctataaca agcagttgt gcccagtatg cccgagcgga ccctgtgcgc gagtggggcca  
421 gcggaggggga gggtaacaag ggggtcgagg cgcttccggg acctcgtaacc caactacaac  
481 cccgacataa tcttcaagga tgaggagaac agcggcgca accgcctgat gacagag

L3 ANSWER 3 OF 8

GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AB018401 GenBank (R)  
GenBank ACC. NO. (GBN): AB018401  
CAS REGISTRY NO. (RN): 218090-26-7  
SEQUENCE LENGTH (SQL): 1491  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 13 Oct 1998  
DEFINITION (DEF): *Homo sapiens* hedgehog gene, exon 1.  
KEYWORDS (ST): hedgehog  
SOURCE: *Homo sapiens* DNA.  
ORGANISM (ORGN): *Homo sapiens*  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;

NUCLEIC ACID COUNT : 345 a 369 c 490 g 28  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): **Human desert hedgehog**  
 gene  
 JOURNAL (SO): Published Only in DataBase (1998) In press  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (04-OCT-1998) to the DDBJ/EMBL/GenBank  
 databases. Genshu Tate, Showa University Fujigaoka  
 Hospital, Department of Surgical Pathology; Fujigaoka  
 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan  
 (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
 Fax:81-45-972-6242)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1491	/organism="Homo sapiens" /db-xref="taxon:9606"
gene	1171..1473	/gene="hedgehog"
exon	1171..1473	/gene="hedgehog" /number=1

SEQUENCE (SEQ):

1 ctcgagggaa cacaggtggg cagtgttggg acatcaagga aggcttctta gaagaaatga  
 61 cttctaaaca aaagaaaattg gacgtggtgc ctctgagatg agatctgagt ggctgaaaat  
 121 ggagccccgg gagtccagag agggagaaaag ctggagaggt gccttagatgg acgtttaagg  
 181 gaagtgtatcc tcacctctta caaagacttt tgagtgtcca ctggcccttca gcagcttcca  
 241 actgagaagt cattcatttg aaaaacagca gctatttagat gcctggcaaa gaagagaagg  
 301 gggaaaaaaagt tggaagtccct aaatgagaca ataagtacca agctctgttc ctggttctgg  
 361 ggaagttcca aaggagactg caaagtttagt agagaaaatgg gcccctgtta tcctcacctc  
 421 ccagtcctgc ttaatgtga atgtgaggag agatggaagt cggggagatc tggggaggac  
 481 tacagagaag ggaggctctg gttgtatgcc caaagggtt ggctggctt gggcagaaaat  
 541 tggaacccat acttccttgg tgacagcgga gggcatggcc tgccaggta ggctttgaga  
 601 gagtaaaaat tccaaattcaa gtatcagagg agggttggtt ggttccaagt ttaagcttgg  
 661 aggttagaagg atgtttaggc agccaaggac tgtaaagcta caagtatttc cttaggcagg  
 721 gtctgcctgg tttccaggat gggacacact tcagtcgcaa aatggaccag cagtgaccgg  
 781 ctagatcccc cgccccgggtg ggaggggggtg ggacggctt gggagaaggg cggagggcgg  
 841 ggccaggggc cacttaaggc ggagtccggta gtccggcgt tctggcagca ccagagtcc  
 901 gcagcagaga cgggtgggc tggcactcac ccacgacccc ccttccctgc tatgtgttt  
 961 tgtcagtagc aggtcctaga caccggccgc cccgtccccgg ggcacgtgg cagagctagc  
 1021 agcagccagg tgcacggagc cacaagagct cttagggcact ctggggcag ctgtgcctgc  
 1081 tgccctctct ggtgcctgtg gagatgccta actgacagga gagtttagtga ggacaagaac  
 1141 gtcctctttt ggccgaggc cgtgtatcc atggctctcc tgaccaatct actgcccctg  
 1201 tgctgcttgg cacttctggc gtcgcctggc cagagctgcg ggccggccg gggccgggtt  
 1261 ggccggcgcc gctatgcgc caagcagctc gtgcgcgtac tctacaagca atttgtgccc  
 1321 ggctgtccag agcggaccct gggcgccagt gggccagcgg aggggagggt ggcaaggggc  
 1381 tccgagcgc tccggacac cgtgcacac tacaaccccg acatcatctt caaggatgag  
 1441 gagaacagtg gagccgaccg cctgatgacc gaggttaagga gggcctctcc c

L3 ANSWER 4 OF 8

GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AB010581S3 GenBank (R)  
 GenBank ACC. NO. (GBN): AB010994  
 CAS REGISTRY NO. (RN): 204280-14-8  
 SEQUENCE LENGTH (SQL): 626  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 14 Feb 1998  
 DEFINITION (DEF): **Homo sapiens hedgehog gene, exon 3 and**  
 complete cds.  
 KEYWORDS (ST): hedgehog

SEGMENT: 3 of 3  
 SOURCE: **Homo sapiens** DNA.  
 ORGANISM (ORGN): **Homo sapiens**  
 NUCLEIC ACID COUNT (NA): 73 a 200 c 236 g 117 t  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): **Human Desert Hedgehog**,  
 third exon  
 JOURNAL (SO): Published Only in DataBase (1998) In press  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank  
 databases. Genshu Tate, Showa University Fujigaoka  
 Hospital, Department of Surgical Pathology; Fujigaoka  
 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan  
 (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
 Fax:81-45-972-6242)

FEATURES (FEAT):

Feature	Key	Location	Qualifier
source	1..626		/organism="Homo sapiens" /db-xref="taxon:9606"
gene	join(AB010581:1..303, AB010993:1..262,1..626)		/gene="hedgehog"
CDS	join(AB010581:1..303, AB010993:1..262,1..626)		/gene="hedgehog"  /codon-start=1 /db-xref="PID:d1025788" /db-xref="PID:g2887457" /translation="MALLTNLLPLCCLALLALPA QSCGPGRGPVRRRYARKQLVPLL YKQFVPGVPERTLGA GASGP AEGRVARGSERFRDLV PNYNPDIIFKDEENSGADR LMTER CKERVN ALAIAVM MNWPGV RL RVTE GWDEDGH HA QDSL HYEGRAL DITTS DRDR NKYG LLAR LAVEAG FDWV YYE S RNH VH VS V KAD NSL A V R AG GCF PGN AT V RL WS GER KGL RE L H R GD W V L A AD A S G R V V P T P V L L F L D R D L Q R R A S F V A V E T E W P P R K L L T P W H L V F A A R G P A P A P G D F A P V F A R R L R A G D S V L A P G G D A L R P A R V A R E E A V G V F A P L T A H G T L L V N D V L A S C Y A V L E S H Q W A H R A F A P L R L L H A G A L L P G G A V Q P T G M H W Y S R L L Y R L A E E L L G"
exon	1..626		/gene="hedgehog" /number=3

SEQUENCE (SEQ):

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1 ataactcaact ggccgtccgg gcggggcggt gctttccggg aaatgcact gtgcgcctgt
61 ggagcggcga gcggaaaggg ctgcggaaac tgccacgcgg agactgggtt ttggcggccg
121 atgcgtcagg ccgggtggtg cccacgcgg tgctgtctt cctggacccg gacttgcacgc
181 gccgggcttc atttgggtct gtggagaccc agtggcctcc acgcaactg ttgtcacgc
241 cctggcaccc ggtgtttgcc gtcgaggccc cggcgccccg gccaggccgac tttgcacccgg
301 tgttcgccg cccgtacgc gctggggact cggtgctggc gcccggccgg gatgcgttcc
361 ggccagcgcg cgtggcccgt gtggcgcggg aggaagccgt gggcgtttc gcgcgcgtca
421 cccgcacccg gacgtctgtg gtgaacgtg tcctggcctc ttgctacgcg gttctggaga
481 gtcaccagtg ggcgcacccgc gcttttgcgg ccttgagact gctgcacgcg ctaggggcgc
541 tgctccccgg cggggccgtc cagccgactg gcatgcattg gtactctcgg ctcccttacc
601 gcttagcgga ggagctactg ggctga

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LOCUS (LOC): AB010581S2 GenBank (R)  
 GenBank ACC. NO. (G): AB010993  
 CAS REGISTRY NO. (RN): 204280-13-7  
 SEQUENCE LENGTH (SQL): 262  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 14 Feb 1998  
 DEFINITION (DEF): **Homo sapiens hedgehog gene, exon 2.**  
 KEYWORDS (ST): hedgehog  
 SEGMENT: 2 of 3  
 SOURCE: **Homo sapiens** DNA.  
 ORGANISM (ORGN): **Homo sapiens**  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; **Homo**  
 NUCLEIC ACID COUNT (NA): 52 a 76 c 84 g 50 t  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): **Human Desert Hedgehog,**  
 second exon  
 JOURNAL (SO): Published Only in DataBase (1998) In press  
 REFERENCE:  
 AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank  
 databases. Genshu Tate, Showa University Fujigaoka  
 Hospital, Department of Surgical Pathology; Fujigaoka  
 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan  
 (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
 Fax:81-45-972-6242)

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..262	/organism="Homo sapiens" /db-xref="taxon:9606"
exon	1..262	/gene="hedgehog" /number=2

**SEQUENCE (SEQ):**

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 1 cgttgtaaagg agcgggtgaa cgctttggcc attggcgtga tgaacatgtg gcccggagtg
 61 cgccctacgag tgactgaggg ctgggacgag gacggccacc acgctcagga ttcaactccac
121 tacgaaggcc gtgctttgga catcaactacg tctgaccgcg accgcaacaa gtatgggttg
181 ctggcgcgccc tcgcagtggaa agccggcttc gactgggtct actacgagtc ccgcaaccac
241 gtccacgtgt cggtcaaagc tg
```

L3 ANSWER 6 OF 8 GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AB010581S1 GenBank (R)  
GenBank ACC. NO. (GBN): AB010581  
CAS REGISTRY NO. (RN): 202961-68-0  
SEQUENCE LENGTH (SQL): 303  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 14 Feb 1998  
DEFINITION (DEF): **Homo sapiens** hedgehog gene, exon 1.  
KEYWORDS (ST): hedgehog  
SEGMENT:  
1 of 3  
SOURCE:  
**Homo sapiens** DNA.  
ORGANISM (ORGN):  
**Homo sapiens**  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; **Homo**  
NUCLEIC ACID COUNT (NA): 51 a 100 c 104 g 48 t  
REFERENCE:  
1 (bases 1 to 303)  
AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
TITLE (TI): **Human Desert Hedgehog**,

JOURNAL (SO): first exon  
Published Only in DataBase ( ) In press  
REFERENCE: 2 (bases 1 to 303)  
AUTHOR (AU): Tate, G.; Endo, Y.; Mitsuya, T.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (20-JAN-1998) to the DDBJ/EMBL/GenBank  
databases. Genshu Tate, Showa University Fujigaoka  
Hospital, Department of Surgical Pathology; Fujigaoka  
1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan  
(E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
Fax:81-45-972-6242)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..303	/organism="Homo sapiens" /db-xref="taxon:9606"
exon	1..303	/gene="hedgehog" /number=1

SEQUENCE (SEQ):

1 atggctctcc tgaccaatct actgcccctg tgctgcttgg cacttctggc gctgccagcc  
61 cagagctgcg ggccggggccg gggggccgggt ggccggcgcc gctatgcgcg caagcagctc  
121 gtgccgcgtac tctacaagca atttggtgccc ggcgtgccag agcggacccct gggccgcgt  
181 gggccagcgg aggggagggt ggcaaggggc tccgagcgct tccgggacact cgtgcccac  
241 tacaaccccg acatcatctt caaggatgag gagaacagtg gagccgaccg cctgatgacc  
301 gag

L3 ANSWER 7 OF 8

GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): AA064660 GenBank (R)  
GenBank ACC. NO. (GBN): AA064660  
CAS REGISTRY NO. (RN): 181404-26-2  
SEQUENCE LENGTH (SQL): 314  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Expressed sequence tag  
DATE (DATE): 23 Dec 1997  
DEFINITION (DEF): zml3f08.s1 Stratagene pancreas (#937208) **Homo**  
sapiens cDNA clone 525543 3' similar to TR:G443942  
G443942 **DESERT HEDGEHOG PRECURSOR.**  
;  
KEYWORDS (ST): EST  
SOURCE: **human.**  
ORGANISM (ORGN): **Homo sapiens**  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; **Homo**

NUCLEIC ACID COUNT (NA): 31 a 100 c 117 g 55 t 11 others

COMMENT:

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent  
plate of this clone contains both **human** and mouse derived  
clones.

Thus, the origin of this clone is uncertain. This caution should be  
kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

Insert Length: 862 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 283.  
 REFERENCE: 1 (bases 1 to 314)  
 AUTHOR (AU): Hillier, L.; Clark, N.; Dubuque, T.; Elliston, K.;  
 Hawkins, M.; Holman, M.; Hultman, M.; Kucaba, T.; Le, M.;  
 Lennon, G.; Marra, M.; Parsons, J.; Rifkin, L.;  
 Rohlfing, T.; Tan, F.; Trevaskis, E.; Waterston, R.;  
 Williamson, A.; Wohldmann, P.; Wilson, R.  
 TITLE (TI): WashU-Merck EST Project  
 JOURNAL (SO): Unpublished (1995)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..314	/organism="Homo sapiens" /note="Organ: pancreas; Vector: pBluescript SK-; Site-1: EcoRI; Site-2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pancreatic adenocarcinoma cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCTGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT /db-xref="GDB:3916972" /db-xref="taxon:9606" /clone="525543" /clone-lib="Stratagene pancreas (#937208)" /lab-host="SOLR cells (kanamycin resistant)"

SEQUENCE (SEQ):

1 ggccggcncc gcgcagngng anntttgcac cgggtttcgc gcgcggcta cgctngggg  
 61 actcggtgtc ggccggccgc ggggatgcgc ttcggccagc gcgcgtggcc cgtgtggcgc  
 121 gggaggaagc cgtggngtng ttcgcgcgc tcaccgcga cgggacgctg ctgtgaacg  
 181 atgtcctggc ctcttgctac gcggttctgg agagtcacca gtgggcgcac cgcttnttg  
 241 ccccccttgag actgctgcac gcgcttagggg cttgtcccc ggcggccgt ccagccgact  
 301 ggaatgcatt tngg

L3 ANSWER 8 OF 8. GENBANK.RTM. COPYRIGHT 1999

LOCUS (LOC): HSU59748 GenBank (R)  
 GenBank ACC. NO. (GBN): U59748  
 CAS REGISTRY NO. (RN): 178296-28-1  
 SEQUENCE LENGTH (SQL): 285  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 4 Jul 1996  
 DEFINITION (DEF): **Human desert hedgehog**  
                   (hDHH) mRNA, partial cds.  
 SOURCE: **human**.  
 ORGANISM (ORGN): **Homo sapiens**  
                   Eukaryota; mitochondrial eukaryotes; Metazoa;  
                   Chordata; Vertebrata; Eutheria; Primates; Catarrhini;  
                   Hominidae; **Homo**  
 NUCLEIC ACID COUNT (NA): 62 a 73 c 92 g 58 t  
 REFERENCE:  
   AUTHOR (AU): Drummond, I.A.  
   TITLE (TI): **Human desert hedgehog**  
   JOURNAL (SO): Unpublished  
 REFERENCE:  
   AUTHOR (AU): Drummond, I.A.  
   TITLE (TI): Direct Submission  
   JOURNAL (SO): Submitted (02-JUN-1996) Renal Unit, Mass. General

## FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..285	/organism="Homo sapiens" /tissue-type="kidney" /dev-stage="15 week fetus"
gene	1..285	/gene="hDHH"
CDS	<1..>285	/gene="hDHH" /note="secreted protein" /codon-start=3 /product="desert hedgehog" /db-xref="PID:g1401272" /translation="IIFKDEENSGADRLMTERCK ERVNALAIAVMNWPGVRLRVTEG WDEDGHHAQDSLHYEGRALDITTSRDRNKYGLL ARLAVEAGFDWVYYGS"

## SEQUENCE (SEQ):

1 atattatttt taaggatgaa gagaacagtg gagccgaccg cctgatgacc gagcgttgt  
61 aggagcgggt gaacgctttg gccattgccg tgatgaacat gtggcccgga gtgcgcctac  
121 gagtgactga gggctgggac gaggacggcc accacgctca ggattcactc cactacgaag  
181 gccgtgctt ggacatcact acgtctgacc gcgaccgcaa caagtatggg ttgctggcgc  
241 gcctcgcagt ggaagccggc tttgactggg tctactacgg atccg

L5 ANSWER 1 OF 1 MEDLINE  
AN 1999030620 MEDLINE  
DN 99030620  
TI Characterization of two patched receptors for the vertebrate hedgehog protein family.  
AU Carpenter D; Stone D M; Brush J; Ryan A; Armanini M; Frantz G; Rosenthal A; de Sauvage F J  
CS Department of Molecular Oncology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA.  
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1998 Nov 10) 95 (23) 13630-4.  
Journal code: PV3. ISSN: 0027-8424.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals; Cancer Journals  
OS GENBANK-AF091501  
EM 199902  
EW 19990204

L5 ANSWER 1 OF 1 MEDLINE

AB The multitransmembrane protein Patched (PTCH) is the receptor for Sonic Hedgehog (Shh), a secreted molecule implicated in the formation of embryonic structures and in tumorigenesis. Current models suggest that binding of Shh to PTCH prevents the normal inhibition of the seven-transmembrane-protein Smoothened (SMO) by PTCH. According to this model, the inhibition of SMO signaling is relieved after mutational inactivation of PTCH in the basal cell nevus syndrome. Recently, PTCH2, a molecule with sequence homology to PTCH, has been identified. To characterize both PTCH molecules with respect to the various **Hedgehog** proteins, we have isolated the **human** PTCH2 gene. Biochemical analysis of PTCH and PTCH2 shows that they both bind to all hedgehog family members with similar affinity and that they can form

a complex with SMO. However, the expression patterns of PTCH and PTCH2 do not fully overlap. While PTCH is expressed throughout the mouse embryo, PTCH2 is found at high levels in the skin and in spermatocytes. Because **Desert** Hedgehog (Dhh) is expressed specifically in the testis and is required for germ cell development, it is likely that PTCH2 mediates its activity *in vivo*. Chromosomal localization of PTCH2 places it on chromosome 1p33-34, a region deleted in some germ cell tumors, raising the possibility that PTCH2 may be a tumor suppressor in Dhh target cells.

Patent No. 5789543

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.  
; APPLICANT: McMahon, Andrew P.  
; APPLICANT: Tabin, Clifford J.  
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
; TITLE OF INVENTION: Proteins and Uses Related Thereto  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,427B  
; FILING DATE: 30-DEC-1993  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-176-427B-4

Query Match 98.7%; Score 828; DB 2; Length 396;  
Best Local Similarity 97.7%; Pred. No. 3.5e-101;  
Matches 172; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPYN 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 23 CGPGRGPVGRRYVRKQLVPLLYKQFVPSMPERTLGASGPAEGRVTRGSERFRDLVPYN 82

Qy 61 PDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGWDLEGHQAQDSLHY 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 83 PDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGWDLEGHQAQDSLHY 142

Qy 121 EGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 176  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 143 EGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 198

; Patent No. 5844079  
; GENERAL INFORMATION:  
; APPLICANT: Ingham, Phillip W.  
; APPLICANT: McMahon, Andrew P.  
; APPLICANT: Tabin, Clifford J.  
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
; TITLE OF INVENTION: Proteins and Uses Related Thereto  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,060A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,427  
; FILING DATE: 30-DEC-1993  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-060A-9

Query Match 98.7%; Score 828; DB 2; Length 396;  
Best Local Similarity 97.7%; Pred. No. 3.5e-101;  
Matches 172; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA\$GPAEGRVARGSERFRDLVPN 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| ||| ||| :||| ||| ||| |||  
Db 23 CGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTLGA\$GPAEGRVTRGSERFRDLVPN 82  
  
Qy 61 PDIIFKDEENSGADRLMTERCKERNALAIAVMNWPGVRLRVTEGWDEDGHHAQDSLHY 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 83 PDIIFKDEENSGADRLMTERCKERNALAIAVMNWPGVRLRVTEGWDEDGHHAQDSLHY 142  
  
Qy 121 EGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 176  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 143 EGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 198

ID R77341 standard; Protein; 475 AA.  
AC R77341;  
DT 14-MAR-1996 (first entry)  
DE Human sonic hedgehog protein.  
KW Human; sonic hedgehog protein; probe; primer; diagnostic;  
KW nervous system disorder; gene therapy; antibody.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT peptide 24. .29  
FT /note= "conserved sequence (R77349)"  
FT misc\_difference 463  
FT /note= "unspecified amino acid"  
PN WO9518856-A1.  
PD 13-JUL-1995.  
PF 30-DEC-1994; U14992.  
PR 30-DEC-1993; US-176427.  
PR 14-DEC-1994; US-356060.  
PA (HARD ) HARVARD COLLEGE.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PI Ingham PW, McMahon AP, Tabin CJ;  
DR WPI; 95-255060/33.  
DR N-PSDB; Q91639.  
PT Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful  
PT to treat degenerative nervous system disorder(s) and in gene  
PT therapy.  
PS Claim 17; Page 143-45; 210pp; English.  
CC The sequence represents a human sonic hedgehog protein, homologous  
CC to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA  
CC isolated from a human fetal lung cDNA library. Probes and primers  
CC derived from the sonic hedgehog gene may be used as diagnostic  
CC agents for neuromuscular, autonomic or central nervous system  
CC disorders, and the gene may also be used in gene therapy.  
CC Antibodies generated from the protein may be used as therapeutic or  
CC research reagents.  
SQ Sequence 475 AA;

Query Match 79.5%; Score 667; DB 1; Length 475;  
Best Local Similarity 75.0%; Pred. No. 3.8e-80;  
Matches 132; Conservative 29; Mismatches 13; Indels 2; Gaps 2;

Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL GAS GPAEGRVARGSERFRDLVPN 60  
Db 24 CGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTL GAS GRYEGKISRNSERFKELT P 81

Qy 61 PDIIFKDEENSGADRLMTERCKERNALAIAVMNWPGVRLRVTEGWDEDGHHAQDSLHY 120  
Db 82 PDIIFKDEENTGADRLMTQRC KDKLNALAI SVMNQWPGVKL RVTEGWDEDGHSEESLHY 141

Qy 121 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 176  
Db 142 EGRAVDITTSDRDRSKYGMMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGG 197

; Patent No. 5759811  
; GENERAL INFORMATION:  
; APPLICANT: Epstein, Ervin  
; APPLICANT: Hu, Zhilan  
; APPLICANT: Bonifas, Jeanette  
; TITLE OF INVENTION: Mutant Human Hedgehog Gene  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/748,591  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 462 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-748-591-4

; Sequence 20, Application PC/TUS9515923  
; GENERAL INFORMATION:  
; APPLICANT: The Johns Hopkins University School of Medicine, et al.  
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES  
; NUMBER OF SEQUENCES: 20  
; FILING DATE: 04-DEC-1995  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 437 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-15923-20

Query Match 79.5%; Score 667; DB 3; Length 437;  
Best Local Similarity 75.0%; Pred. No. 7.2e-80;  
Matches 132; Conservative 29; Mismatches 13; Indels 2; Gaps 2;

Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPYN 60  
Db 25 CGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPYN 82

Qy 61 PDIIFKDEENSGADRLMTERCKERNALAIAVMNMWPGVRLRVTEGWDLEGHHAQDSLHY 120  
Db 83 PDIIFKDEENTGADRLMTQRCKDKLNALAI SVMNQWPGVKLRVTEGWDLEGHSEESLHY 142

Qy 121 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 176  
Db 143 EGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKAENSAAKSGG 198

W096/17924 A3  
W096/16668 11

Desert hedgehog protein precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 10-Sep-1997  
C;Accession: B49425  
R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McMahon, A.P.  
Cell 75, 1417-1430, 1993  
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.  
A;Reference number: A49425  
A;Accession: B49425  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-396 <ECH>  
A;Cross-references: GB:X76292; NID:g443941; PID:g443942  
C;Genetics:  
A;Gene: Dhh

Query Match 98.7%; Score 828; DB 2; Length 396;  
Best Local Similarity 97.7%; Pred. No. 4.7e-84;  
Matches 172; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL GAS GPA EGRV ARG SER F R D L V P N Y N 60  
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Qy 61 PDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGWD E D G H H A Q D S L H Y 120  
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ID 043323 PRELIMINARY; PRT; 396 AA.  
AC 043323;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE HEDGEHOG.  
GN HEDGEHOG.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TATE G., ENDO Y., MITSUYA T.;  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL; AB010994; D1025788; -.  
DR EMBL; AB010581; D1025788; JOINED.  
DR EMBL; AB010993; D1025788; JOINED.  
SQ SEQUENCE 396 AA; 43577 MW; 8200C40F CRC32;

Query Match 99.8%; Score 837; DB 2; Length 396;  
Best Local Similarity 99.4%; Pred. No. 7.1e-84;  
Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 23 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPN 82  
  
Qy 61 PDIIFKDEENSGADRLMTERCKERNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHY 120  
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Db 83 PDIIFKDEENSGADRLMTERCKERNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHY 142  
  
Qy 121 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHIHVSVKADNSLAVRAGG 176  
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Db 143 EGRALDITTSDRDRNKGLLARLAVEAGFDWVYYESRNHVSVKADNSLAVRAGG 198

AC W79594; **COMPARISON TO SEQ ID NO:2**  
DT 02-FEB-1999 (first entry)  
DE Human Desert hedgehog protein.  
KW Desert hedgehog; HuDHH; human; monoclonal antibody.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Protein 1..176  
FT /label= Mat\_protein  
PN EP-874048-A2.  
PD 28-OCT-1998.  
PF 24-APR-1998; 303187.  
PR 14-APR-1998; JP-117873.  
PR 25-APR-1997; JP-121578.  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Ariyasu T, Nakamura S, Orita K;  
DR WPI; 98-544642/47.  
DR N-PSDB; V62394.  
PT Human Desert hedgehog protein - and corresponding DNA and monoclonal antibody  
PT  
PS Claim 3; Page 22-23; 39pp; English.  
CC This is the amino acid sequence of a precursor of a novel human  
CC Desert hedgehog protein, as deduced from a cDNA clone (see V62394)  
CC derived from cell line ARH-77 (ATCC CRL-1621). The mature form  
CC (see W79593) of the hedgehog protein is also claimed, as are a  
CC monoclonal antibody (MAb) that recognises the protein, a process  
CC for producing the protein, and a method for detecting the protein.  
CC The hedgehog protein is useful in establishment of hybridomas which  
CC produce antibodies recognising the protein, and the MAb is useful  
CC for detecting and purifying the protein. The hedgehog protein,  
CC DNA and MAb can be used to elucidate hereditary morphological  
CC abnormalities in humans to establish their treatments and diagnoses.  
SQ Sequence 374 AA;

Claim 4 = 100%  
100:3

Query Match 100.0%; Score 1805; DB 1; Length 374;  
Best Local Similarity 100.0%; Pred. No. 6e-197;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPYN 60  
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Qy 61 PDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHY 120  
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Qy 361 YSRLLYRLAEELLG 374  
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Db 361 YSRLLYRLAEELLG 374

; Patent No. 5789543: COMPARISON TO SEQ ID NO:2  
; GENERAL INFORMATION:  
; APPLICANT: Ingham, Phillip W.  
; APPLICANT: McMahon, Andrew P.  
; APPLICANT: Tabin, Clifford J.  
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
; TITLE OF INVENTION: Proteins and Uses Related Thereto  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,427B  
; FILING DATE: 30-DEC-1993  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

Query Match 97.6%; Score 1761; DB 2; Length 396;  
Best Local Similarity 97.3%; Pred. No. 1.9e-191;  
Matches 364; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

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Db 323 GVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLHALGALLPGGAVQPTGMHW 382

Qy 361 YSRLLYRLAEELLG 374  
Db 383 YSRLLYRLAEELMG 396

AC 043323; COMPARISON TO SEQ ID NO:2  
01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE HEDGEHOG.  
GN HEDGEHOG.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TATE G., ENDO Y., MITSUYA T.;  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL; AB010994; D1025788; -.  
DR EMBL; AB010581; D1025788; JOINED.  
DR EMBL; AB010993; D1025788; JOINED.  
SQ SEQUENCE 396 AA; 43577 MW; 8200C40F CRC32;

Query Match 99.7%; Score 1800; DB 2; Length 396;  
Best Local Similarity 99.5%; Pred. No. 1.5e-159;  
Matches 372; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 GVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLHALGALLPGGAVQPTGMHW 360  
Db 323 GVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLHALGALLPGGAVQPTGMHW 382

Qy 361 YSRLLYRLAELLG 374  
Db 383 YSRLLYRLAELLG 396

LOCUS (LOC) : AB010581S3 GenBank (R)

GenBank ACC. NO. (GBN) : AB010994

CAS REGISTRY NO. (RN) : 204280-14-8

SEQUENCE LENGTH (SQL) : 626

5 MOLECULE TYPE (CI) : DNA; linear

DIVISION CODE (CI) : Primates

DATE (DATE) : 14 Feb 1998

DEFINITION (DEF) : \*\*\*Homo\*\*\* sapiens hedgehog gene, exon 3 and complete cds.

10 KEYWORDS (ST) : hedgehog

SEGMENT: 3 of 3

SOURCE: \*\*\*Homo\*\*\* sapiens DNA.

ORGANISM (ORGN) : \*\*\*Homo sapiens\*\*\*  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;

15 Eutheria; Primates; Catarrhini; Hominidae;  
\*\*\*Homo\*\*\*

NUCLEIC ACID COUNT (NA): 73 a 200 c 236 g 117 t

REFERENCE: 1 (bases 1 to 626)

AUTHOR (AU) : Tate,G.; Endo,Y.; Mitsuya,T.

20 TITLE (TI) : \*\*\*Human\*\*\* \*\*\*Desert\*\*\* \*\*\*Hedgehog\*\*\* ,  
third exon

JOURNAL (SO) : Published Only in DataBase (1998) In press

REFERENCE: 2 (bases 1 to 626)

AUTHOR (AU) : Tate,G.; Endo,Y.; Mitsuya,T.

25 TITLE (TI) : Direct Submission

JOURNAL (SO) : Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank  
databases. Genshu Tate, Showa University Fujigaoka  
Hospital, Department of Surgical Pathology; Fujigaoka  
1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan

30 (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
Fax:81-45-972-6242)

FEATURES (FEAT) :

Feature Key	Location	Qualifier
source	1..626	/organism="Homo sapiens"

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20        ARVARVAREEAVGVFAPLTAHGTL
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121 atgcgtcagg ccgggtgggt cccacgcggg tgctgctttt cctggaccgg gacttgcagc
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481 gtcaccagtg ggcgcaccgc gctttgccc ccttgagact gctgcacgcg ctaggggcgc
541 tgctccccgg cggggccgtc cagccgactg gcatgcattt gtaactctcggtt ctcctctacc

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601 gcttagcgga ggagctactg ggctga

## SUMMARY:

BSUM(14)

The . . . The gene is located on human chromosome 2pter, and has the genome database accession number GDB:511203. A partial sequence of **human desert hedgehog** (hDHH) mRNA, has the Genbank Accession number U59748.

=&gt; d fro

US PAT NO: 5,759,811 [IMAGE AVAILABLE] L7: 1 of 1  
DATE ISSUED: Jun. 2, 1998  
TITLE: Mutant human hedgehog gene  
INVENTOR: Ervin Epstein, Orinda, CA  
              Zhilan Hu, San Francisco, CA  
              Jeanette Bonifas, San Francisco, CA  
ASSIGNEE: The Regents of the University of California, Oakland, CA  
              (U.S. corp.)  
APPL-NO: 08/748,591  
DATE FILED: Nov. 13, 1996  
INT-CL: [6] C12P 21/06; C12N 15/00; C07K 1/00; C07H 21/02  
US-CL-ISSUED: 435/69.1, 320.1; 530/350; 536/23.1; 935/22  
US-CL-CURRENT: 435/69.1, 320.1; 530/350; 536/23.1  
SEARCH-FLD: 435/69.1, 320.1; 530/350; 536/23.1; 935/22  
REF-CITED:

## OTHER PUBLICATIONS

Oro et al. (1997) Basal cell carcinoma in mice overexpressing sonic hedgehog. *Science* 276: 817-821, May 2, 1997.

Fan et al. (1997) Induction to basal cell carcinoma features in transgenic human skin expressing sonic hedgehog. *Nature Medicine* 3 (7): 788-792, Jun. 1997.

Rudinger (1976) Characteristics of the amino acid components of a peptide hormone sequence. In: *Peptide Hormones*, Ed. J. A. Parsons, University Park Press, Baltimore, MD, pp. 1-7, Jan. 1976.

Gailani et al. (1996) The role of the human homologue of Drosophila patched in sporadic basal cell carcinomas. *Nature Genetics* 14: 78-81, Sep. 14, 1998.

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Hahn et al. (1996) Mutations of the human homolog of Drosophila patched in the nevoid basal cell carcinoma syndrome. *Cell* 85: 841-851, Jun. 14, 1996.

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Stone et al. (1996) The tumor-suppressor gene patched encodes a candidate receptor for Sonic hedgehog. *Nature* 384: 129-134, Nov. 14, 1996.

Ogura et al. (1996) Evidence that Shh cooperates with a retinoic acid inducible co-factor to establish ZPA-like activity. *Development* 122: 537-542, Feb. 1996.

ART-UNIT: 184

mDHH to hDHH of SEQ ID NO:7 = 91% identity

Comparison of mouse DHH of patent with SEQ ID NO:6

AR021199

LOCUS AR021199 1190 bp DNA PAT 04-DEC-1998  
 DEFINITION Sequence 3 from patent US 5789543.  
 5 ACCESSION AR021199  
 NID g3975814  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 10 Unclassified.  
 REFERENCE 1 (bases 1 to 1190)  
 AUTHORS Ingham, P.W., McMahon, A.P. and Tabin, C.J.  
 TITLE Vertebrate embryonic pattern-inducing proteins and uses related thereto  
 15 JOURNAL Patent: US 5789543-A 3 04-AUG-1998;  
 FEATURES Location/Qualifiers  
 source 1..1190  
 /organism="unknown"  
 20 BASE COUNT 194 a 371 c 399 g 226 t  
 ORIGIN

Query Match 81.1%; Score 964; DB 6; Length 1190;  
 Best Local Similarity 88.2%; Pred. No. 5.3e-160;  
 25 Matches 1048; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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 Qy 841 CCCGCGCCAGGCACCTTGACCCGGTGGTTCGCCGCGCCGGCTACCGCCTGGGACTCGGTG 900  
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 Db 841 CCTGCTCCAGGTGACTTGCACCCGGTGGTTCGCCGCGCCGCTAACGTGCTGGCAGCTCGGTG 900  
 30 Qy 901 CTGGCGCCCGGGGGATGCGCTTCGGCCAGCGCGGTGGCCCGTGTGGCGCGGGAGGAA 960  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 901 CTGGCTCCCGGGGGACGCGCTCCAGCGCGCGTAGCCCGCGTGGCGCGAGGAA 960  
 35 Qy 961 GCGTGGCGTGGTTCGCCGCTCACCGCGCACGGGACGCTGGTGAACGATGTCCTG 1020  
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 Db 961 GCGTGGCGTGGTTCGCCGCTCACCGCGTAGCGCACGGGACGCTGGTCAACGACGTCCTC 1020  
 Qy 1021 GCCTCTGCTACCGGGTCTGGAGAGTCACCAAGTGGCGCACCGCGCTTTGCCCTTG 1080  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 40 Db 1021 GCCTCTGCTACCGGGTCTAGAGAGTCACCAAGTGGCCCACCGCGCTTGCCCTTG 1080  
 Qy 1081 AGACTGCTGCACGCGCTAGGGCGCTGCTCCCCGGCGGGCCGTCCAGCCGACTGGCATG 1140  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1081 CGGCTGCTGCACGCGCTGGGCTCTGCTCCCTGGGGTGCAGTCCAGCCGACTGGCATG 1140  
 45 Qy 1141 CATTGGTACTCTGGCTCCTACCGCTAGCGGAGGAGCTACTGGC 1188  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1141 CATTGGTACTCTGGCTCCTTACCGCTGGCGAGGAGTTAATGGC 1188  
 50

SEQ ID NO:7  
 = nt. 49 → 596

51 mismatch  
 548 ⇒ 918 identity

LOCUS (LOC) : AB010581S3 GenBank (R)  
 GenBank ACC. NO. (GBN) : AB010994  
 CAS REGISTRY NO. (RN) : 204280-14-8  
 SEQUENCE LENGTH (SQL) : 626  
 5 MOLECULE TYPE (CI) : DNA; linear  
 DIVISION CODE (CI) : Primates  
 DATE (DATE) : 14 Feb 1998  
 DEFINITION (DEF) : \*\*\*Homo\*\*\* sapiens hedgehog gene, exon 3 and  
 complete cds.  
 10 KEYWORDS (ST) : hedgehog  
 SEGMENT: 3 of 3  
 SOURCE: \*\*\*Homo\*\*\* sapiens DNA.  
 ORGANISM (ORGN) : \*\*\*Homo sapiens\*\*\*  
 15 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae;  
 \*\*\*Homo\*\*\*  
 NUCLEIC ACID COUNT (NA) : 73 a 200 c 236 g 117 t  
 REFERENCE: 1 (bases 1 to 626)  
 AUTHOR (AU) : Tate,G.; Endo,Y.; Mitsuya,T.  
 20 TITLE (TI) : \*\*\*Human\*\*\* \*\*\*Desert\*\*\* \*\*\*Hedgehog\*\*\* ,  
 third exon  
 JOURNAL (SO) : Published Only in DataBase (1998) In press  
 REFERENCE: 2 (bases 1 to 626)  
 AUTHOR (AU) : Tate,G.; Endo,Y.; Mitsuya,T.  
 25 TITLE (TI) : Direct Submission  
 JOURNAL (SO) : Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank  
 databases. Genshu Tate, Showa University Fujigaoka  
 Hospital, Department of Surgical Pathology; Fujigaoka  
 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan  
 30 (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,  
 Fax:81-45-972-6242)

FEATURES (FEAT) :

	Feature Key	Location	Qualifier
35	source	1..626	/organism="Homo sapiens" /db-xref="taxon:9606"
	gene	join(AB010581:1..303, AB010993:1..262,1..626)	/gene="hedgehog"
40	CDS	join(AB010581:1..303, AB010993:1..262,1..626)	/codon-start=1 /db-xref="PID:d1025788" /db-xref="PID:g2887457" /translation="MALLTNLLPLCCLALLALPA QSCGPGRGPVGRRYARKQLVPLL YKQFVPGVPERTLIGASGPAEGRVARGSERFRDLV PNYNPDIIFKDEENSGADRLMTER CKERVNALAIAVMMWPGVRLRVTEGWDEDGHHA QDSLHYEGRALDITTSRDRNKYG LLARLAVEAGFDWVYYESRNHVVSVKADNSLAV RAGGCFCGNATVRLWSGERKGLRE LHRGDWVLAADASGRVVPTPVLLFLDRDLQRRAS FVAVETEWPPRKLLTPWHLVFAA"
45			
50			

5 exon 1..626 RGPAPAPGDFAPVFARRL RAGDSVLAPGGDALRP  
ARVARVAREEAVGVFAPLTAHGL  
LVNDVLASCYAVLESHQWAHRAFAPLRLLHALGA  
LLPGGAVQPTGMHWYSRLLYRLAE ELLG"  
/gene="hedgehog"  
/number=3

SEQUENCE (SEQ) :

10 1 ataaactact ggccgtccgg gcggggcggt gctttccggg aaatgcaact gtgcgcctgt  
61 61 ggagccgcga gcggaaaggg ctgcgggaac tgccacgcgg agactgggtt ttggccggccg  
121 121 atgcgtcagg ccgggtggtg cccacgcgg tgctgcttt cctggaccgg gacttgcagc  
181 181 gccgggcttc atttgtggct gtggagaccc agtggcctcc acgcaaactg ttgctcacgc  
241 241 cctggcacct ggtgtttgcc gctcgagggc cggcccccgc gccaggcgac tttgcaccgg  
301 301 tttcgccgc ccggctacgc gctggggact cgggtctggc gcccggcggt gatgcgttc  
361 361 ggccagcgcc cgtggccgt gtggccggg aggaagccgt gggcgtgtc gcgcgcgtca  
421 421 ccgcgcacgg gacgctgctg gtgaacgatg tcctggcctc ttgctacgcg gtttggaga  
481 481 gtcaccagtg ggccacccgc gctttgcc ccttgagact gctgcacgcg ctaggggcgc  
541 541 tgctccccgg cggggccgtc cagccgactg gcatgcattt gtactctcggt ctcctctacc  
601 601 gcttagcgga ggagctactg ggctga

20

LOCUS (LOC) : HSU59748 GenBank (R)  
 GenBank ACC. NO. (GBN) : U59748  
 CAS REGISTRY NO. (RN) : 178296-28-1  
 SEQUENCE LENGTH (SQL) : 285  
 5 MOLECULE TYPE (CI) : mRNA; linear  
 DIVISION CODE (CI) : Primates  
 DATE (DATE) : 4 Jul 1996  
 DEFINITION (DEF) : \*\*\*Human\*\*\* \*\*\*desert\*\*\* \*\*\*hedgehog\*\*\*  
 (hDHH) mRNA, partial cds.  
 10 SOURCE:  
 ORGANISM (ORGN) : \*\*\*human\*\*\* .  
 \*\*\*Homo sapiens\*\*\*  
 Eukaryotae; mitochondrial eukaryotes; Metazoa;  
 Chordata; Vertebrata; Eutheria; Primates; Catarrhini;  
 Hominidae; \*\*\*Homo\*\*\*  
 15 NUCLEIC ACID COUNT (NA) : 62 a 73 c 92 g 58 t  
 REFERENCE:  
 AUTHOR (AU) : Drummond, I.A.  
 TITLE (TI) : \*\*\*Human\*\*\* \*\*\*desert\*\*\* \*\*\*hedgehog\*\*\*  
 JOURNAL (SO) : Unpublished  
 20 REFERENCE:  
 AUTHOR (AU) : Drummond, I.A.  
 TITLE (TI) : Direct Submission  
 JOURNAL (SO) : Submitted (02-JUN-1996) Renal Unit, Mass. General  
 Hospital, 149 13th street, Charlestown, MA 02129, USA  
 25 FEATURES (FEAT) :  

Feature Key	Location	Qualifier
source	1..285	/organism="Homo sapiens" /tissue-type="kidney" /dev-stage="15 week fetus"
gene	1..285	/gene="hDHH"
CDS	<1..>285	/gene="hDHH" /note="secreted protein" /codon-start=3 /product="desert hedgehog" /db-xref="PID:g1401272" /translation="IIFKDEENSGADRLMTERCK ERVNALAIAVMNWPGVRLRVTEG WDEDGHHAQDSLHYEGRALDITTSRDRNKYGLL ARLAVEAGFDWVYYGS"

 30  
 35  
 40  
 SEQUENCE (SEQ) :  
 45 1 atattatttt taaggatgaa gagaacagtg gagccgaccg cctgatgacc gagcgttcta  
     61 aggagcgggt gaacgctttg gccattgcgg tgatgaacat gtggcccgga gtgcgcctac  
     121 gagtgactga gggctggac gaggacggcc accacgctca ggattcactc cactacgaag  
     181 gccgtgcttt ggacatcact acgtctgacc gcgaccgcaa caagtatggg ttgctggcgc  
     241 gcctcgcagt ggaagccggc tttgactggg tctactacgg atccg

Corresponds to aa 63 → 156 of SEQ ID NO:7